

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/697,206A

DATE: 06/20/2001
 TIME: 14:36:16

Input Set : A:\Seqlist.txt
 Output Set: N:\CRF3\06202001\I697206A.raw

ENTERED

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4 <110> APPLICANT: Daniel E.H. Afar
5      Arthur B. Raitano
6      Rene S. Hubert
7      Steve Chappell Mitchell
8      Aya Jakobovits
10 <120> TITLE OF INVENTION: NOVEL GENE UPREGULATED IN CANCERS OF THE
11      PROSTATE
13 <130> FILE REFERENCE: 129.21-US-U1
15 <140> CURRENT APPLICATION NUMBER: 09/697,206A
C--> 16 <141> CURRENT FILING DATE: 2001-06-04
18 <150> PRIOR APPLICATION NUMBER: 60/162,364
19 <151> PRIOR FILING DATE: 1999-10-28
21 <160> NUMBER OF SEQ ID NOS: 26
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 3585
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo Sapiens
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32 atcctgctgt tctggaaagt cgtggatctg gccaacaaga aggtgggaca gttgcacgaa      120
33 gtgcttagtta gaccggatca gtggaaactg acggaggact gcaaagaaga aactaaaata      180
34 gacgtcgaaa gcctgtccctc ggcgtcgca gctggaccaag ccctccgaca gtttaaccag      240
35 tcagtgagca atgaactgaa tattggatgaa gggacttcct tctgtctctg tactgatggg      300
36 cagttcatg tcaggccaaat cctgcacatccct gaggcttcca agaagaatgt actattacct      360
37 gaatgcttctt attcctttt tgatcttcga aaagaattca agaaatgttg ccctggttca      420
38 cctgatattg acaaactgga ctttgccaca atgacagagt atttaaatatt tgagaagagt      480
39 agttcagttct ctcgatatgg agcctctcaa gttgaagata tgggaatat aatttagca      540
40 atgatttcag agccttataa tcacagggtt tcagatccag agagagtggaa ttacaagttt      600
41 gaaagtggaa cttgcagcaa gatggaaactt attgatgata acaccgtgt cagggcacga      660
42 ggtttaccat ggcagttctc agatcaagat attgcaagat tcttcaaagg actcaatatt      720
43 gccaaggggag gtgcagcact ttgtctgaat gctcagggtc gaagggacgg agaagctctg      780
44 gttaggtttg taagtgagga gcacccgagac ctgcactac agaggccacaa acatcacatg      840
45 gggacccgggt atattgaggt ttacaaagca acagggtggaa atttccttaa aattgctgg      900
46 ggtacttcca atgaggtagc ccagttctc tccaaaggaaa atcaagtcat tgttcgcatg      960
47 cgggggctcc ctttcacggc cacagctgaa gaagggtgg ctttcttgg acagcattgc      1020
48 cctattactg gggaaagga agcattccct tttgtcacct acccgatgg taggccaaca      1080
49 gggacgctt ttgtccctt tgccgtgag gaatatgcac agaatgcgtt gaggaagcat      1140
50 aaagacttgtt tggtaaaatg atacattgaa ctcttcagga gcacagcagc tgaagttcag      1200
51 caggtgctga atcgatctc ctcggccccct ctcattccac ttccaaacccc tcccttatt      1260
52 ccagttactac ctcagcaatt ttgtccccct acaaatttta gagactgtat acgccttcga      1320
53 ggtctccct atgcagccac aatttggggac atcctggatt ttctgggggaa gttcgccaca      1380
54 gatattcgta ctcatgggtt tcacatgggtt ttgaatcacc agggccggccc atcaggagat      1440
55 gccttatacc agatgaagtc tgcggacaga gcatttatgg ctgcacagaa gtgtcataaa      1500
56 aaaaacatga aggacagata tggtaagtc tttcagttt cagctgagga gatgaacttt      1560
57 gtgttaatgg gggcactttt aatcgaaat ggcttatccc caccggccatg cctgtctcc      1620
58 ccctcctaca catttcacgc tcctgctgca gttattccca cagaagctgc catttaccag      1680

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59	ccctctgtga	ttttgaatcc	acgagcactg	cagccctcca	cagcgtacta	cccagcaggc	1740	
60	actcagctct	tcatgaacta	cacagcgtac	tatccca	ccccaggttc	gcctaata	1800	
61	cttggctact	tccctacagc	tgctaatctt	agcggtgtcc	ctccacagcc	tggcacggtg	1860	
62	gtcagaatgc	agggcctggc	ctacaatact	ggagtaagg	aaattcttaa	cttcttccaa	1920	
63	ggttaccagt	atgcaaccga	ggatggactt	atacacacaa	atgaccaggc	caggactcta	1980	
64	cccaaagaat	gggtttgtat	ttaagggcc	cagcagttag	aacatcctca	gaaaagaagt	2040	
65	gtttgaaaga	tgtatggtga	tcttgaaaacc	tccagacaca	agaaaaacttc	tagcaaattc	2100	
66	aggggaagtt	tgtctacact	caggctgcag	tat	ttcagc	aaacttgatt	ggacaaaacgg	2160
67	gcctgtgcct	tatctttgg	tggagtgaaa	aaatttgagc	tagtgaagcc	aaatcgtaac	2220	
68	ttacagcaag	cagcatgcag	catacctggc	tcttgcgtga	ttgcaaatag	gcattaaaa	2280	
69	tgtgaatttg	gaatcagatg	tccattac	ttccagttaa	agtggcatca	tagtgtttc	2340	
70	ctaagttta	agtcttggat	aaaaactcca	ccagtgtcta	ccatctccac	catgaactct	2400	
71	gttaaggaag	cttcattttt	gtatattccc	gctctttct	cttcattttc	ctgtcttctg	2460	
72	cataatcatg	ccttcttgct	aagtaattca	agcataagat	cttggataaa	taaaatcaca	2520	
73	atcttaggag	aaagaataaa	attgttattt	tcccagtctc	ttggccatga	tgatatctta	2580	
74	tgattaaaaa	caaattaaat	tttaaaacac	ctgaagataa	attagaagaa	atttgtgcacc	2640	
75	ctccacaaaa	catacaaagt	ttaaaagttt	ggatctttt	ctcagcagt	atcagttgt	2700	
76	aataatgaat	tagggccaa	aatgc	aaaaatgaa	gcagctacat	gtagtttagta	2760	
77	atttctagtt	tgaactgtaa	ttgaatattt	tggcttcata	tgtatttattt	tatattgtac	2820	
78	tttttcatt	attgatggtt	tggactttaa	taagagaaat	tccatagttt	ttaatatccc	2880	
79	agaagtgaga	caatttgaac	agtgtattct	agaaaacaat	acactaactg	aacagaagt	2940	
80	aatgcttata	tatattatga	tagccttaaa	ccttttct	cta	atgcctt	3000	
81	taattataac	cttttaaagc	ataggactat	agt	cagcatg	ctagactgag	3060	
82	tgtatcaatt	agaacaggt	ctgatgctgt	cagt	ttttaa	cactatgtt	3120	
83	atgctataaa	agtcaat	tagacactag	ctag	tactgc	tgcctcatgt	3180	
84	aaaacaggat	ttcattaagt	gcattgaat	tggatattt	tca	agttac	3240	
85	cttgc	ttga	atgcaatgcc	gtgcagattt	atgaggctgc	tat	ttctgtgc	3300
86	tactttaaca	ccttaaagg	agaagcaa	at	ttccttct	tca	gctgact	3360
87	ctttaactgc	aataggaaga	aaaaaaa	ggtt	ttgtgt	aaaatgg	ataactgg	3420
88	cttaagatcg	aaaagaaatt	tctgtatact	tga	tgcctta	agatgccc	3480	
89	agctctgaaa	gactttaaga	taggcagtaa	tgcttactac	aatactactg	agttttgt	3540	
90	gagttaacat	ttgataataa	aa	cttgcctg	tttaatctca	aaaaa	3585	

92 <210> SEQ ID NO: 2

93 <211> LENGTH: 517

94 <212> TYPE: PRT

95 <213> ORGANISM: Homo Sapiens

97 <400> SEQUENCE: 2

98	Met	Thr	Glu	Tyr	Leu	Asn	Phe	Glu	Lys	Ser	Ser	Ser	Val	Ser	Arg	Tyr
99	1				5				10				15			
100	Gly	Ala	Ser	Gln	Val	Glu	Asp	Met	Gly	Asn	Ile	Ile	Leu	Ala	Met	Ile
101					20				25				30			
102	Ser	Glu	Pro	Tyr	Asn	His	Arg	Phe	Ser	Asp	Pro	Glu	Arg	Val	Asn	Tyr
103					35				40				45			
104	Lys	Phe	Glu	Ser	Gly	Thr	Cys	Ser	Lys	Met	Glu	Leu	Ile	Asp	Asp	Asn
105									55				60			
106	Thr	Val	Val	Arg	Ala	Arg	Gly	Leu	Pro	Trp	Gln	Ser	Ser	Asp	Gln	Asp
107	65				70				75				80			
108	Ile	Ala	Arg	Phe	Phe	Lys	Gly	Leu	Asn	Ile	Ala	Lys	Gly	Gly	Ala	Ala
109					85				90				95			

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110 Leu Cys Leu Asn Ala Gln Gly Arg Arg Asn Gly Glu Ala Leu Val Arg
 111 100 105 110
 112 Phe Val Ser Glu Glu His Arg Asp Leu Ala Leu Gln Arg His Lys His
 113 115 120 125
 114 His Met Gly Thr Arg Tyr Ile Glu Val Tyr Lys Ala Thr Gly Glu Asp
 115 130 135 140
 116 Phe Leu Lys Ile Ala Gly Gly Thr Ser Asn Glu Val Ala Gln Phe Leu
 117 145 150 155 160
 118 Ser Lys Glu Asn Gln Val Ile Val Arg Met Arg Gly Leu Pro Phe Thr
 119 165 170 175
 120 Ala Thr Ala Glu Glu Val Val Ala Phe Phe Gly Gln His Cys Pro Ile
 121 180 185 190
 122 Thr Gly Gly Lys Glu Gly Ile Leu Phe Val Thr Tyr Pro Asp Gly Arg
 123 195 200 205
 124 Pro Thr Gly Asp Ala Phe Val Leu Phe Ala Cys Glu Glu Tyr Ala Gln
 125 210 215 220
 126 Asn Ala Leu Arg Lys His Lys Asp Leu Leu Gly Lys Arg Tyr Ile Glu
 127 225 230 235 240
 128 Leu Phe Arg Ser Thr Ala Ala Glu Val Gln Gln Val Leu Asn Arg Phe
 129 245 250 255
 130 Ser Ser Ala Pro Leu Ile Pro Leu Pro Thr Pro Pro Ile Ile Pro Val
 131 260 265 270
 132 Leu Pro Gln Gln Phe Val Pro Pro Thr Asn Val Arg Asp Cys Ile Arg
 133 275 280 285
 134 Leu Arg Gly Leu Pro Tyr Ala Ala Thr Ile Glu Asp Ile Leu Asp Phe
 135 290 295 300
 136 Leu Gly Glu Phe Ala Thr Asp Ile Arg Thr His Gly Val His Met Val
 137 305 310 315 320
 138 Leu Asn His Gln Gly Arg Pro Ser Gly Asp Ala Phe Ile Gln Met Lys
 139 325 330 335
 140 Ser Ala Asp Arg Ala Phe Met Ala Ala Gln Lys Cys His Lys Lys Asn
 141 340 345 350
 142 Met Lys Asp Arg Tyr Val Glu Val Phe Gln Cys Ser Ala Glu Glu Met
 143 355 360 365
 144 Asn Phe Val Leu Met Gly Gly Thr Leu Asn Arg Asn Gly Leu Ser Pro
 145 370 375 380
 146 Pro Pro Cys Leu Ser Pro Pro Ser Tyr Thr Phe Pro Ala Pro Ala Ala
 147 385 390 395 400
 148 Val Ile Pro Thr Glu Ala Ala Ile Tyr Gln Pro Ser Val Ile Leu Asn
 149 405 410 415
 150 Pro Arg Ala Leu Gln Pro Ser Thr Ala Tyr Tyr Pro Ala Gly Thr Gln
 151 420 425 430
 152 Leu Phe Met Asn Tyr Thr Ala Tyr Tyr Pro Ser Pro Pro Gly Ser Pro
 153 435 440 445
 154 Asn Ser Leu Gly Tyr Phe Pro Thr Ala Ala Asn Leu Ser Gly Val Pro
 155 450 455 460
 156 Pro Gln Pro Gly Thr Val Val Arg Met Gln Gly Leu Ala Tyr Asn Thr
 157 465 470 475 480
 158 Gly Val Lys Glu Ile Leu Asn Phe Phe Gln Gly Tyr Gln Tyr Ala Thr

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159	485	490	495
160	Glu Asp Gly Leu Ile His Thr Asn Asp Gln Ala Arg Thr Leu Pro Lys		
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162	Glu Trp Val Cys Ile		
163	515		
165	<210> SEQ ID NO: 3		
166	<211> LENGTH: 14		
167	<212> TYPE: DNA		
168	<213> ORGANISM: Artificial Sequence		
170	<220> FEATURE:		
171	<223> OTHER INFORMATION: Primer		
173	<400> SEQUENCE: 3		
174	ttttgatcaa gctt		14
176	<210> SEQ ID NO: 4		
177	<211> LENGTH: 42		
178	<212> TYPE: DNA		
179	<213> ORGANISM: Artificial Sequence		
181	<220> FEATURE:		
182	<223> OTHER INFORMATION: Adaptor		
184	<400> SEQUENCE: 4		
185	ctaatacgac tcactatagg gtcgagcgg ccgcggggc ag		42
187	<210> SEQ ID NO: 5		
188	<211> LENGTH: 12		
189	<212> TYPE: DNA		
190	<213> ORGANISM: Artificial Sequence		
192	<220> FEATURE:		
193	<223> OTHER INFORMATION: Adaptor		
195	<400> SEQUENCE: 5		
196	ggcccggtcct ag		12
198	<210> SEQ ID NO: 6		
199	<211> LENGTH: 40		
200	<212> TYPE: DNA		
201	<213> ORGANISM: Artificial Sequence		
203	<220> FEATURE:		
204	<223> OTHER INFORMATION: Adaptor		
206	<400> SEQUENCE: 6		
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209	<210> SEQ ID NO: 7		
210	<211> LENGTH: 10		
211	<212> TYPE: DNA		
212	<213> ORGANISM: Artificial Sequence		
214	<220> FEATURE:		
215	<223> OTHER INFORMATION: Adaptor		
217	<400> SEQUENCE: 7		
218	cggctcctag		10
220	<210> SEQ ID NO: 8		
221	<211> LENGTH: 22		
222	<212> TYPE: DNA		
223	<213> ORGANISM: Artificial Sequence		

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225 <220> FEATURE:
 226 <223> OTHER INFORMATION: Primer
 228 <400> SEQUENCE: 8
 229 ctaatacgac tcactatagg gc 22
 231 <210> SEQ ID NO: 9
 232 <211> LENGTH: 22
 233 <212> TYPE: DNA
 234 <213> ORGANISM: Artificial Sequence
 236 <220> FEATURE:
 237 <223> OTHER INFORMATION: Primer
 239 <400> SEQUENCE: 9
 240 tcgagcggcc gcccgggcag ga 22
 242 <210> SEQ ID NO: 10
 243 <211> LENGTH: 20
 244 <212> TYPE: DNA
 245 <213> ORGANISM: Artificial Sequence
 247 <220> FEATURE:
 248 <223> OTHER INFORMATION: Primer
 250 <400> SEQUENCE: 10
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 253 <210> SEQ ID NO: 11
 254 <211> LENGTH: 25
 255 <212> TYPE: DNA
 256 <213> ORGANISM: Homo Sapiens
 258 <400> SEQUENCE: 11
 259 atatcgccgc gctcgctgc gacaa 25
 261 <210> SEQ ID NO: 12
 262 <211> LENGTH: 26
 263 <212> TYPE: DNA
 264 <213> ORGANISM: Homo Sapiens
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 269 <210> SEQ ID NO: 13
 270 <211> LENGTH: 24
 271 <212> TYPE: DNA
 272 <213> ORGANISM: Artificial Sequence
 274 <220> FEATURE:
 275 <223> OTHER INFORMATION: Primer
 277 <400> SEQUENCE: 13
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 280 <210> SEQ ID NO: 14
 281 <211> LENGTH: 24
 282 <212> TYPE: DNA
 283 <213> ORGANISM: Artificial Sequence
 285 <220> FEATURE:
 286 <223> OTHER INFORMATION: Primer
 288 <400> SEQUENCE: 14
 289 ggagatggta gacactggtg gagt 24
 291 <210> SEQ ID NO: 15

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/697,206A

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L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date